## Wild boars as a source of antimicrobial resistant *Escherichia coli*

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To reveal wild boars as a reservoir of antimicrobial resistance 332 faecal samples were collected from individual wild boars shot during 42 hunts within two seasons (2012/13 and 2013/14) in 34 regional forests scattered over the whole territory of Poland. Direct streak on MacConkey agar was used for isolation of indicator, commensal of Escherichia(E.) coli, whereas ceforaxime-supplemented (2 mg/L) MacConkey gave estimates on prevalence of cephalosporin-resistant E. coli. PCR targeting uspA gene was used for identification of presumptive E. coli followed by MIC determination using Sensititre® EUVMS2 and EUVSEC2 (cephalosporin resistant isolates) plates. MICs were interpreted according to EUCAST epidemiological cut-off values. A total of 278 commensal E. coli were retrieved (83,7% recovery rate) along with nine cephalosporin resistant isolates (2,7%; 1,0 ÷ 4,5%). Commensal isolates conferred resistance against 10 of 14 antimicrobials tested reaching the highest values for sulfamethoxazole (8.3 %), ampicillin (2.5%), streptomycin (2.2%), trimethoprim, ciprofloxacin, and tetracycline (1.8% each). Chloramphenicol, nalidixic acid, gentamicin, and kanamycin resistances ranged between 0.4 % and 1.1%. Two Ciprofloxacin-NWT and Nalidixic acid-WT isolates carried PMQR genes identified further with sequencing as qnrS1 gene (or qnrS3, the product too short to discriminate). Of the nine cephalosporin-resistant isolates the mechanism resistance was identified as $bla_{CMY-2}$ (N=6), and three true-ESBLs, including $bla_{CTX-M-15}$ and $bla_{CTX-M-1}$(N=2). CTX-M-15(+) E. coli carried also qnrS1 gene. A variety of plasmids were observed in cephalosporin resistant isolates (data not shown). PBRT done on one of CMY-2(+) isolates classified the resistance plasmid to IncI1-alpha incomparability group. None of the cephalosporin resistant isolates harbored pathogenicity markers (PCR) typical for enteropathogenic, enteroaggregative, enterotoxigenic, enteroinvasive or verotoxin-producing E. coli. The results prove wild boars as environmental pool of cephalosporin and PMQR resistance genes. Their origin cannot be defined, since they might easily originate from the environment itself, or from farm animals, since wild boars are often foraging on agricultural areas. The results draw attention to environmental aspects of spread of resistance.

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